

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 1, 2004, 10:20:52 ; Search time 63 Seconds
(without alignments)
1024.941 Million cell updates/sec

Title: US-10-772-985-12
Perfect score: 976
Sequence: 1 MDWPHSLLFLLAISIFLAPS.....GPCRQRVVMETIAVGCTCIF 180

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	976	100.0	180	2 AAY28236	Aay28236 Mouse int
2	976	100.0	180	2 AAW85617	Aaw85617 Murine Zc
3	976	100.0	180	2 AAY22198	Aay22198 Murine ED
4	976	100.0	180	3 AAB07687	Aab07687 A murine
5	976	100.0	180	3 AAB07593	Aab07593 A murine
6	976	100.0	180	7 ADB31992	Adb31992 Mouse int
7	976	100.0	180	8 ADR13794	Adr13794 Murine in
8	970	99.4	179	4 AAE10951	Aae10951 Mouse Zcy
9	970	99.4	179	6 ABB99362	Abb99362 Amino aci
10	970	99.4	179	6 ABG71975	Abg71975 Mouse ful

11	872	89.3	160	2	AAW85645	Aaw85645	Murine	Zc
12	872	89.3	160	4	AAE10967	Aae10967	Human	Zcy
13	872	89.3	160	6	ABB99378	Abb99378	Amino	aci
14	872	89.3	160	6	ABG71991	Abg71991	Human	Zcy
15	868	88.9	180	2	AAZ28235	Aay28235	Human	int
16	868	88.9	180	2	AAW85615	Aaw85615	Human	Zcy
17	868	88.9	180	2	AAZ22197	Aay22197	Human	EDI
18	868	88.9	180	2	AAZ41762	Aay41762	Human	PRO
19	868	88.9	180	2	AAW97350	Aaw97350	Interleuk	
20	868	88.9	180	3	AAB33443	Aab33443	Human	PRO
21	868	88.9	180	3	AAZ44459	Aay44459	Human	Int
22	868	88.9	180	3	AAB44318	Aab44318	Human	PRO
23	868	88.9	180	3	AAB18671	Aab18671	Amino	aci
24	868	88.9	180	3	AAB18755	Aab18755	A human	i
25	868	88.9	180	3	AAZ93973	Aay93973	Amino	aci
26	868	88.9	180	4	AAE10950	Aae10950	Human	Zcy
27	868	88.9	180	4	AAU12394	Aau12394	Human	PRO
28	868	88.9	180	4	AAU04950	Aau04950	Human	Int
29	868	88.9	180	4	AAB49894	Aab49894	Human	PRO
30	868	88.9	180	4	AAB50920	Aab50920	Human	PRO
31	868	88.9	180	4	AAG65242	Aag65242	Human	cel
32	868	88.9	180	6	ABB99361	Abb99361	Amino	aci
33	868	88.9	180	6	ABO17838	Abo17838	Novel	hum
34	868	88.9	180	6	ABO25264	Abo25264	Novel	hum
35	868	88.9	180	6	ABU81092	Abu81092	Human	PRO
36	868	88.9	180	6	ABU72270	Abu72270	Novel	hum
37	868	88.9	180	6	ABU66792	Abu66792	Human	PRO
38	868	88.9	180	6	ABU84950	Abu84950	Human	sec
39	868	88.9	180	6	ABU59873	Abu59873	Novel	sec
40	868	88.9	180	6	ABU61148	Abu61148	Human	PRO
41	868	88.9	180	6	ABO25063	Abo25063	Human	sec
42	868	88.9	180	6	ABU89697	Abu89697	Human	int
43	868	88.9	180	6	ABU80417	Abu80417	Human	sec
44	868	88.9	180	6	ABU67068	Abu67068	Human	sec
45	868	88.9	180	6	ABG71974	Abg71974	Human	ful

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OM protein - protein search, using sw model

Run on: December 1, 2004, 10:25:13 ; Search time 37.0588 Seconds
(without alignments)
322.116 Million cell updates/sec

Title: US-10-772-985-12
Perfect score: 976
Sequence: 1 MDWPHSLLFLLAISIFLAPS.....GPCRQRVVMTIavgctCIF 180

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	976	100.0	180	4	US-09-620-956-12	Sequence 12, Appl
2	976	100.0	180	4	US-09-611-152-12	Sequence 12, Appl
3	976	100.0	180	4	US-09-480-297A-4	Sequence 4, Appli
4	976	100.0	180	4	US-09-631-531-12	Sequence 12, Appl
5	970	99.4	179	4	US-09-794-705A-7	Sequence 7, Appli
6	872	89.3	160	4	US-09-620-956-39	Sequence 39, Appl
7	872	89.3	160	4	US-09-611-152-39	Sequence 39, Appl
8	872	89.3	160	4	US-09-794-705A-24	Sequence 24, Appl
9	872	89.3	160	4	US-09-631-531-39	Sequence 39, Appl
10	868	88.9	180	4	US-09-231-788-2	Sequence 2, Appli
11	868	88.9	180	4	US-09-620-956-2	Sequence 2, Appli
12	868	88.9	180	4	US-09-611-152-2	Sequence 2, Appli

13	868	88.9	180	4	US-09-794-705A-2	Sequence 2, Appli
14	868	88.9	180	4	US-09-747-259-2	Sequence 2, Appli
15	868	88.9	180	4	US-09-816-744-2	Sequence 2, Appli
16	868	88.9	180	4	US-09-631-531-2	Sequence 2, Appli
17	868	88.9	180	4	US-10-140-002-446	Sequence 446, App
18	864	88.5	180	4	US-09-480-297A-2	Sequence 2, Appli
19	857	87.8	158	4	US-09-620-956-40	Sequence 40, Appl
20	857	87.8	158	4	US-09-611-152-40	Sequence 40, Appl
21	857	87.8	158	4	US-09-794-705A-25	Sequence 25, Appl
22	857	87.8	158	4	US-09-631-531-40	Sequence 40, Appl
23	793	81.2	160	4	US-09-620-956-19	Sequence 19, Appl
24	793	81.2	160	4	US-09-620-956-23	Sequence 23, Appl
25	793	81.2	160	4	US-09-611-152-19	Sequence 19, Appl
26	793	81.2	160	4	US-09-611-152-23	Sequence 23, Appl
27	793	81.2	160	4	US-09-794-705A-14	Sequence 14, Appl
28	793	81.2	160	4	US-09-794-705A-18	Sequence 18, Appl
29	793	81.2	160	4	US-09-631-531-19	Sequence 19, Appl
30	793	81.2	160	4	US-09-631-531-23	Sequence 23, Appl
31	790	80.9	160	4	US-09-620-956-17	Sequence 17, Appl
32	790	80.9	160	4	US-09-620-956-20	Sequence 20, Appl
33	790	80.9	160	4	US-09-611-152-17	Sequence 17, Appl
34	790	80.9	160	4	US-09-611-152-20	Sequence 20, Appl
35	790	80.9	160	4	US-09-794-705A-12	Sequence 12, Appl
36	790	80.9	160	4	US-09-794-705A-15	Sequence 15, Appl
37	790	80.9	160	4	US-09-631-531-17	Sequence 17, Appl
38	790	80.9	160	4	US-09-631-531-20	Sequence 20, Appl
39	789	80.8	160	4	US-09-620-956-14	Sequence 14, Appl
40	789	80.8	160	4	US-09-620-956-16	Sequence 16, Appl
41	789	80.8	160	4	US-09-611-152-14	Sequence 14, Appl
42	789	80.8	160	4	US-09-611-152-16	Sequence 16, Appl
43	789	80.8	160	4	US-09-794-705A-9	Sequence 9, Appli
44	789	80.8	160	4	US-09-794-705A-11	Sequence 11, Appl
45	789	80.8	160	4	US-09-631-531-14	Sequence 14, Appl

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OM protein - protein search, using sw model

Run on: December 1, 2004, 10:31:58 ; Search time 51.8824 Seconds
(without alignments)
1237.264 Million cell updates/sec

Title: US-10-772-985-12
Perfect score: 976
Sequence: 1 MDWPHSLLFLLAISIFLAPS.....GPCRQRVVMETIAVGCTCIF 180

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
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No.	Score	Match	Length	DB	ID	Description
1	976	100.0	180	10	US-09-774-381-4	Sequence 4, Appli
2	976	100.0	180	14	US-10-253-159-12	Sequence 12, Appl
3	976	100.0	180	14	US-10-340-042-12	Sequence 12, Appl
4	976	100.0	180	14	US-10-366-791-4	Sequence 4, Appli
5	976	100.0	180	16	US-10-742-220-4	Sequence 4, Appli
6	976	100.0	180	16	US-10-772-985-12	Sequence 12, Appl
7	970	99.4	179	9	US-09-794-705A-7	Sequence 7, Appli
8	970	99.4	179	17	US-10-472-916A-7	Sequence 7, Appli
9	872	89.3	160	9	US-09-794-705A-24	Sequence 24, Appl
10	872	89.3	160	14	US-10-253-159-39	Sequence 39, Appl
11	872	89.3	160	14	US-10-340-042-39	Sequence 39, Appl
12	872	89.3	160	16	US-10-772-985-39	Sequence 39, Appl
13	872	89.3	160	17	US-10-472-916A-24	Sequence 24, Appl
14	868	88.9	180	9	US-09-731-816-8	Sequence 8, Appli
15	868	88.9	180	9	US-09-794-705A-2	Sequence 2, Appli
16	868	88.9	180	9	US-09-854-280-1	Sequence 1, Appli
17	868	88.9	180	9	US-09-854-208-1	Sequence 1, Appli
18	868	88.9	180	9	US-09-978-295A-470	Sequence 470, App
19	868	88.9	180	9	US-09-978-697-470	Sequence 470, App
20	868	88.9	180	9	US-09-874-503-2	Sequence 2, Appli
21	868	88.9	180	9	US-09-978-192A-470	Sequence 470, App
22	868	88.9	180	9	US-09-999-832A-470	Sequence 470, App
23	868	88.9	180	10	US-09-320-713-8	Sequence 8, Appli
24	868	88.9	180	10	US-09-816-744-2	Sequence 2, Appli
25	868	88.9	180	10	US-09-978-189-470	Sequence 470, App
26	868	88.9	180	10	US-09-747-259-2	Sequence 2, Appli
27	868	88.9	180	10	US-09-978-608A-470	Sequence 470, App
28	868	88.9	180	10	US-09-978-585A-470	Sequence 470, App
29	868	88.9	180	10	US-09-978-191A-470	Sequence 470, App
30	868	88.9	180	10	US-09-978-403A-470	Sequence 470, App
31	868	88.9	180	10	US-09-978-564A-470	Sequence 470, App
32	868	88.9	180	10	US-09-999-833A-470	Sequence 470, App
33	868	88.9	180	10	US-09-908-827-2	Sequence 2, Appli
34	868	88.9	180	10	US-09-981-915A-470	Sequence 470, App
35	868	88.9	180	10	US-09-978-824-470	Sequence 470, App
36	868	88.9	180	10	US-09-918-585A-470	Sequence 470, App
37	868	88.9	180	10	US-09-999-834A-470	Sequence 470, App
38	868	88.9	180	10	US-09-978-423A-470	Sequence 470, App
39	868	88.9	180	10	US-09-978-193A-470	Sequence 470, App
40	868	88.9	180	10	US-09-999-830A-470	Sequence 470, App
41	868	88.9	180	10	US-09-774-381-2	Sequence 2, Appli
42	868	88.9	180	10	US-09-978-757A-470	Sequence 470, App
43	868	88.9	180	10	US-09-978-187B-470	Sequence 470, App
44	868	88.9	180	10	US-09-978-643A-470	Sequence 470, App
45	868	88.9	180	10	US-09-978-375A-470	Sequence 470, App

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 1, 2004, 10:21:23 ; Search time 102.176 Seconds
(without alignments)
1013.613 Million cell updates/sec

Title: US-10-772-985-12
Perfect score: 976
Sequence: 1 MDWPHSLFLFLLAISIFLAPS.....GPCRQRVVMETIAVGCTCIF 180

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match	Length				
1	976	100.0	180	1	I17B_MOUSE	Q9qxt6	mus musculu
2	924	94.7	178	1	I17B_MESAU	Q9eqi6	mesocricetu
3	868	88.9	180	1	I17B_HUMAN	Q9uhf5	homo sapien
4	864	88.5	180	2	Q6IAG3	Q6iag3	homo sapien
5	864	88.5	180	2	CAG33473	Cag33473	homo sapi
6	593	60.8	111	2	Q9EQI7	Q9eqi7	rattus norv
7	487.5	49.9	203	2	Q6DIY0	Q6diy0	xenopus tro
8	203	20.8	205	2	Q8K4C4	Q8k4c4	mus musculu
9	190	19.5	202	1	I17D_HUMAN	Q8tad2	homo sapien
10	171	17.5	196	2	Q8K599	Q8k599	mus musculu
11	169	17.3	206	2	Q70I20	Q70i20	oncorhynchu
12	169	17.3	206	2	CAE45584	Cae45584	oncorhync
13	168.5	17.3	197	1	I17C_HUMAN	Q9p0m4	homo sapien
14	168.5	17.3	197	2	AAH69152	Aah69152	homo sapi
15	160.5	16.4	194	2	Q8K4C5	Q8k4c5	mus musculu
16	155	15.9	171	2	Q6L5M6	Q6l5m6	ciona intes

17	153	15.7	153	2	Q8K4C3	Q8k4c3 mus musculu
18	153	15.7	161	2	Q7TNI7	Q7tni7 mus musculu
19	153	15.7	161	2	AAQ88439	Aaq88439 mus muscu
20	148.5	15.2	153	1	I17F_HUMAN	Q96pd4 homo sapien
21	148.5	15.2	163	2	Q6NSI0	Q6nsi0 homo sapien
22	148.5	15.2	163	2	AAH70124	Aah70124 homo sapi
23	147.5	15.1	171	2	Q6L5M5	Q6l5m5 ciona intes
24	146	15.0	155	1	IL17_HUMAN	Q16552 homo sapien
25	146	15.0	155	2	AAH67503	Aah67503 homo sapi
26	146	15.0	155	2	AAH67504	Aah67504 homo sapi
27	146	15.0	155	2	AAH67505	Aah67505 homo sapi
28	143	14.7	169	2	Q7T1P7	Q7t1p7 gallus gall
29	139	14.2	155	2	Q6NZ94	Q6nz94 homo sapien
30	139	14.2	155	2	AAH66253	Aah66253 homo sapi
31	133.5	13.7	151	1	VG13_SHV21	P24916 saimiriine
32	131.5	13.5	151	1	VG13_SHV2C	O40633 saimiriine
33	131.5	13.5	151	2	Q778B0	Q778b0 saimiriine
34	131.5	13.5	151	2	CAC84308	Cac84308 saimiriin
35	130.5	13.4	141	2	Q95L56	Q95l56 bos taurus
36	130.5	13.4	186	2	Q6L5M4	Q6l5m4 ciona intes
37	124.5	12.8	153	2	Q8VHC9	Q8vhc9 mus musculu
38	124.5	12.8	169	2	Q8VHH8	Q8vhh8 mus musculu
39	124	12.7	150	1	IL17_RAT	Q61453 rattus norv
40	123.5	12.7	177	1	I17E_HUMAN	Q9h293 homo sapien
41	123.5	12.7	177	2	AAH69565	Aah69565 homo sapi
42	118.5	12.1	158	1	IL17_MOUSE	Q62386 mus musculu
43	118.5	12.1	158	2	BAC30590	Bac30590 mus muscu
44	105.5	10.8	2212	2	Q7Q112	Q7q112 anopheles g
45	104	10.7	146	2	Q70I21	Q70i21 oncorhynchu

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 1, 2004, 10:20:52 ; Search time 56 Seconds
(without alignments)
1024.941 Million cell updates/sec

Title: US-10-772-985-39
Perfect score: 872
Sequence: 1 HPRNTKGKRKGQGRPSPLAP.....GPCRQRVVMETIAVGCTCIF 160

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	ID	Description
	1	872	100.0	160	2	AAW85645	Aaw85645 Murine Zc
	2	872	100.0	160	4	AAE10967	Aae10967 Human Zcy
	3	872	100.0	160	6	ABB99378	Abb99378 Amino aci
	4	872	100.0	160	6	ABG71991	Abg71991 Human Zcy
	5	872	100.0	180	2	AAY28236	Aay28236 Mouse int
	6	872	100.0	180	2	AAW85617	Aaw85617 Murine Zc
	7	872	100.0	180	2	AAY22198	Aay22198 Murine ED
	8	872	100.0	180	3	AAB07687	Aab07687 A murine
	9	872	100.0	180	3	AAB07593	Aab07593 A murine
	10	872	100.0	180	7	ADB31992	Adb31992 Mouse int

11	872	100.0	180	8	ADR13794	Adr13794	Murine in
12	866	99.3	179	4	AAE10951	Aae10951	Mouse Zcy
13	866	99.3	179	6	ABB99362	Abb99362	Amino aci
14	866	99.3	179	6	ABG71975	Abg71975	Mouse ful
15	857	98.3	158	2	AAW85646	Aaw85646	Murine Zc
16	857	98.3	158	4	AAE10968	Aae10968	Human Zcy
17	857	98.3	158	6	ABB99379	Abb99379	Amino aci
18	857	98.3	158	6	ABG71992	Abg71992	Human Zcy
19	793	90.9	160	2	AAW85623	Aaw85623	Human Zcy
20	793	90.9	160	2	AAW85627	Aaw85627	Human Zcy
21	793	90.9	160	4	AAE10961	Aae10961	Human Zcy
22	793	90.9	160	4	AAE10957	Aae10957	Human Zcy
23	793	90.9	160	6	ABB99368	Abb99368	Amino aci
24	793	90.9	160	6	ABB99372	Abb99372	Amino aci
25	793	90.9	160	6	ABG71985	Abg71985	Human Zcy
26	793	90.9	160	6	ABG71981	Abg71981	Human Zcy
27	790	90.6	160	2	AAW85621	Aaw85621	Human Zcy
28	790	90.6	160	2	AAW85624	Aaw85624	Human Zcy
29	790	90.6	160	4	AAE10958	Aae10958	Human Zcy
30	790	90.6	160	4	AAE10955	Aae10955	Human Zcy
31	790	90.6	160	6	ABB99369	Abb99369	Amino aci
32	790	90.6	160	6	ABB99366	Abb99366	Amino aci
33	790	90.6	160	6	ABG71982	Abg71982	Human Zcy
34	790	90.6	160	6	ABG71979	Abg71979	Human Zcy
35	789	90.5	160	2	AAW85618	Aaw85618	Human Zcy
36	789	90.5	160	2	AAW85620	Aaw85620	Human Zcy
37	789	90.5	160	4	AAE10952	Aae10952	Human Zcy
38	789	90.5	160	4	AAE10954	Aae10954	Human Zcy
39	789	90.5	160	4	AAG65243	Aag65243	Human cel
40	789	90.5	160	6	ABB99365	Abb99365	Amino aci
41	789	90.5	160	6	ABB99363	Abb99363	Amino aci
42	789	90.5	160	6	ABG71976	Abg71976	Human Zcy
43	789	90.5	160	6	ABG71978	Abg71978	Human Zcy
44	789	90.5	175	3	AAy44484	Aay44484	Human Int
45	789	90.5	180	2	AAy28235	Aay28235	Human int

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OM protein - protein search, using sw model

Run on: December 1, 2004, 10:25:13 ; Search time 32.9412 Seconds
(without alignments)
322.116 Million cell updates/sec

Title: US-10-772-985-39
Perfect score: 872
Sequence: 1 HPRNTKGKRKGQGRPSPLAP.....GPCRQRVVMETIAVGCTCIF 160

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	872	100.0	160	4	US-09-620-956-39
2	872	100.0	160	4	US-09-611-152-39
3	872	100.0	160	4	US-09-794-705A-24
4	872	100.0	160	4	US-09-631-531-39
5	872	100.0	180	4	US-09-620-956-12
6	872	100.0	180	4	US-09-611-152-12
7	872	100.0	180	4	US-09-480-297A-4
8	872	100.0	180	4	US-09-631-531-12
9	866	99.3	179	4	US-09-794-705A-7
10	857	98.3	158	4	US-09-620-956-40
11	857	98.3	158	4	US-09-611-152-40
12	857	98.3	158	4	US-09-794-705A-25

13	857	98.3	158	4	US-09-631-531-40	Sequence 40, Appl
14	793	90.9	160	4	US-09-620-956-19	Sequence 19, Appl
15	793	90.9	160	4	US-09-620-956-23	Sequence 23, Appl
16	793	90.9	160	4	US-09-611-152-19	Sequence 19, Appl
17	793	90.9	160	4	US-09-611-152-23	Sequence 23, Appl
18	793	90.9	160	4	US-09-794-705A-14	Sequence 14, Appl
19	793	90.9	160	4	US-09-794-705A-18	Sequence 18, Appl
20	793	90.9	160	4	US-09-631-531-19	Sequence 19, Appl
21	793	90.9	160	4	US-09-631-531-23	Sequence 23, Appl
22	790	90.6	160	4	US-09-620-956-17	Sequence 17, Appl
23	790	90.6	160	4	US-09-620-956-20	Sequence 20, Appl
24	790	90.6	160	4	US-09-611-152-17	Sequence 17, Appl
25	790	90.6	160	4	US-09-611-152-20	Sequence 20, Appl
26	790	90.6	160	4	US-09-794-705A-12	Sequence 12, Appl
27	790	90.6	160	4	US-09-794-705A-15	Sequence 15, Appl
28	790	90.6	160	4	US-09-631-531-17	Sequence 17, Appl
29	790	90.6	160	4	US-09-631-531-20	Sequence 20, Appl
30	789	90.5	160	4	US-09-620-956-14	Sequence 14, Appl
31	789	90.5	160	4	US-09-620-956-16	Sequence 16, Appl
32	789	90.5	160	4	US-09-611-152-14	Sequence 14, Appl
33	789	90.5	160	4	US-09-611-152-16	Sequence 16, Appl
34	789	90.5	160	4	US-09-794-705A-9	Sequence 9, Appli
35	789	90.5	160	4	US-09-794-705A-11	Sequence 11, Appl
36	789	90.5	160	4	US-09-631-531-14	Sequence 14, Appl
37	789	90.5	160	4	US-09-631-531-16	Sequence 16, Appl
38	789	90.5	180	4	US-09-231-788-2	Sequence 2, Appli
39	789	90.5	180	4	US-09-620-956-2	Sequence 2, Appli
40	789	90.5	180	4	US-09-611-152-2	Sequence 2, Appli
41	789	90.5	180	4	US-09-794-705A-2	Sequence 2, Appli
42	789	90.5	180	4	US-09-747-259-2	Sequence 2, Appli
43	789	90.5	180	4	US-09-816-744-2	Sequence 2, Appli
44	789	90.5	180	4	US-09-631-531-2	Sequence 2, Appli
45	789	90.5	180	4	US-10-140-002-446	Sequence 446, App

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OM protein - protein search, using sw model

Run on: December 1, 2004, 10:31:58 ; Search time 46.1176 Seconds
(without alignments)
1237.264 Million cell updates/sec

Title: US-10-772-985-39
Perfect score: 872
Sequence: 1 HPRNTKGKRKGQGRPSPLAP.....GPCRQRVVMEITAVGCTCIF 160

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	%
Result	Query

No.	Score	Match	Length	DB	ID	Description
1	872	100.0	160	9	US-09-794-705A-24	Sequence 24, Appl
2	872	100.0	160	14	US-10-253-159-39	Sequence 39, Appl
3	872	100.0	160	14	US-10-340-042-39	Sequence 39, Appl
4	872	100.0	160	16	US-10-772-985-39	Sequence 39, Appl
5	872	100.0	160	17	US-10-472-916A-24	Sequence 24, Appl
6	872	100.0	180	10	US-09-774-381-4	Sequence 4, Appli
7	872	100.0	180	14	US-10-253-159-12	Sequence 12, Appl
8	872	100.0	180	14	US-10-340-042-12	Sequence 12, Appl
9	872	100.0	180	14	US-10-366-791-4	Sequence 4, Appli
10	872	100.0	180	16	US-10-742-220-4	Sequence 4, Appli
11	872	100.0	180	16	US-10-772-985-12	Sequence 12, Appl
12	866	99.3	179	9	US-09-794-705A-7	Sequence 7, Appli
13	866	99.3	179	17	US-10-472-916A-7	Sequence 7, Appli
14	857	98.3	158	9	US-09-794-705A-25	Sequence 25, Appl
15	857	98.3	158	14	US-10-253-159-40	Sequence 40, Appl
16	857	98.3	158	14	US-10-340-042-40	Sequence 40, Appl
17	857	98.3	158	16	US-10-772-985-40	Sequence 40, Appl
18	857	98.3	158	17	US-10-472-916A-25	Sequence 25, Appl
19	793	90.9	160	9	US-09-794-705A-14	Sequence 14, Appl
20	793	90.9	160	9	US-09-794-705A-18	Sequence 18, Appl
21	793	90.9	160	14	US-10-253-159-19	Sequence 19, Appl
22	793	90.9	160	14	US-10-253-159-23	Sequence 23, Appl
23	793	90.9	160	14	US-10-340-042-19	Sequence 19, Appl
24	793	90.9	160	14	US-10-340-042-23	Sequence 23, Appl
25	793	90.9	160	16	US-10-772-985-19	Sequence 19, Appl
26	793	90.9	160	16	US-10-772-985-23	Sequence 23, Appl
27	793	90.9	160	17	US-10-472-916A-14	Sequence 14, Appl
28	793	90.9	160	17	US-10-472-916A-18	Sequence 18, Appl
29	790	90.6	160	9	US-09-794-705A-12	Sequence 12, Appl
30	790	90.6	160	9	US-09-794-705A-15	Sequence 15, Appl
31	790	90.6	160	14	US-10-253-159-17	Sequence 17, Appl
32	790	90.6	160	14	US-10-253-159-20	Sequence 20, Appl
33	790	90.6	160	14	US-10-340-042-17	Sequence 17, Appl
34	790	90.6	160	14	US-10-340-042-20	Sequence 20, Appl
35	790	90.6	160	16	US-10-772-985-17	Sequence 17, Appl
36	790	90.6	160	16	US-10-772-985-20	Sequence 20, Appl
37	790	90.6	160	17	US-10-472-916A-12	Sequence 12, Appl
38	790	90.6	160	17	US-10-472-916A-15	Sequence 15, Appl
39	789	90.5	160	9	US-09-794-705A-9	Sequence 9, Appli
40	789	90.5	160	9	US-09-794-705A-11	Sequence 11, Appl
41	789	90.5	160	14	US-10-253-159-14	Sequence 14, Appl
42	789	90.5	160	14	US-10-253-159-16	Sequence 16, Appl
43	789	90.5	160	14	US-10-340-042-14	Sequence 14, Appl
44	789	90.5	160	14	US-10-340-042-16	Sequence 16, Appl
45	789	90.5	160	16	US-10-772-985-14	Sequence 14, Appl

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OM protein - protein search, using sw model

Run on: December 1, 2004, 10:24:48 ; Search time 28.2353 Seconds
(without alignments)
545.228 Million cell updates/sec

Title: US-10-772-985-39
Perfect score: 872
Sequence: 1 HPRNTKGKRKGQGRPSPLAP.....GPCRQRVVMETIAVGCTCIF 160

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	133.5	15.3		151	1	B45351	immediate-early pr
2	124	14.2		150	2	I49623	cytotoxic T-lympho
3	116.5	13.4		147	2	JC4628	cytotoxic T-lympho
4	101	11.6		206	2	T25139	hypothetical prote
5	90.5	10.4		148	2	T21334	hypothetical prote
6	83.5	9.6		162	2	T32515	hypothetical prote
7	81.5	9.3		494	2	AD3255	l-sorbose dehydrog
8	81	9.3		775	2	T45238	probable transfera
9	80	9.2	1480		2	S48440	poly(A)-specific r
10	79	9.1	768		2	A87722	protein ZC123.1 [i
11	78.5	9.0	326		2	G96812	protein F3F9.6 [im
12	78.5	9.0	2180		2	A47651	zinc-finger protei
13	77.5	8.9	175		1	A60010	early E1A 20K prot
14	77	8.8	552		2	T25195	hypothetical prote

15	76.5	8.8	509	2	S48856	finger protein pcg
16	76.5	8.8	1234	2	T30160	hypothetical prote
17	75.5	8.7	1820	2	A55494	latent transformin
18	75	8.6	1051	1	JW0051	serine/threonine-s
19	74.5	8.5	106	2	T44238	B9 protein [import
20	74.5	8.5	1140	2	D88690	protein F41H10.3 [
21	74.5	8.5	1299	2	T47182	hypothetical prote
22	74	8.5	342	2	T05217	hypothetical prote
23	74	8.5	666	2	T35864	hypothetical prote
24	73.5	8.4	328	2	D83559	probable transcrip
25	73.5	8.4	1265	2	T51498	hypothetical prote
26	73	8.4	460	2	D75610	probable peroxidase
27	72.5	8.3	270	2	F84255	hypothetical prote
28	72.5	8.3	431	2	T01557	hypothetical prote
29	72.5	8.3	2492	1	MNWVTD	nonstructural poly
30	72	8.3	145	2	T04942	G10 protein homolo
31	72	8.3	655	2	T22448	probable peroxidase
32	72	8.3	2187	2	T30826	nascent polypeptid
33	72	8.3	2327	2	T42630	aggrecan - bovine
34	72	8.3	2531	2	T31070	notch homolog - se
35	71.5	8.2	460	2	D96971	stage V sporulatio
36	71.5	8.2	1953	2	S63244	BN11 protein - yea
37	71.5	8.2	2492	1	A44213	nonstructural poly
38	71.5	8.2	2492	1	C44213	nonstructural poly
39	71	8.1	509	2	G83442	probable 3-hydroxy
40	71	8.1	597	2	C82367	aminopeptidase P V
41	71	8.1	2284	1	GNVVG	genome polyprotein
42	70.5	8.1	429	2	S34224	cyclin B - long-ta
43	70.5	8.1	434	2	F84605	hypothetical prote
44	70.5	8.1	435	2	T46443	hypothetical prote
45	70.5	8.1	546	2	T19680	hypothetical prote

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OM protein - protein search, using sw model

Run on: December 1, 2004, 10:21:23 ; Search time 90.8235 Seconds
(without alignments)
1013.613 Million cell updates/sec

Title: US-10-772-985-39
Perfect score: 872
Sequence: 1 HPRNTKGKRKGQGRPSPLAP.....GPCRQRVVMTIavgctCIF 160

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	872	100.0	180	1 I17B_MOUSE	Q9qxt6 mus musculu
2	824	94.5	178	1 I17B_MESAU	Q9eqi6 mesocricetu
3	789	90.5	180	1 I17B_HUMAN	Q9uhf5 homo sapien
4	785	90.0	180	2 Q6IAG3	Q6iag3 homo sapien
5	785	90.0	180	2 CAG33473	Cag33473 homo sapi
6	593	68.0	111	2 Q9EQI7	Q9eqi7 rattus norv
7	474	54.4	203	2 Q6DIY0	Q6diy0 xenopus tro
8	188	21.6	205	2 Q8K4C4	Q8k4c4 mus musculu
9	177	20.3	202	1 I17D_HUMAN	Q8tad2 homo sapien
10	168.5	19.3	206	2 Q70I20	Q70i20 oncorhynchu
11	168.5	19.3	206	2 CAE45584	Cae45584 oncorhync
12	163.5	18.8	197	1 I17C_HUMAN	Q9p0m4 homo sapien
13	163.5	18.8	197	2 AAH69152	Aah69152 homo sapi
14	160.5	18.4	194	2 Q8K4C5	Q8k4c5 mus musculu
15	156	17.9	196	2 Q8K599	Q8k599 mus musculu
16	155	17.8	171	2 Q6L5M6	Q6l5m6 ciona intes

17	153	17.5	153	2	Q8K4C3	Q8k4c3 mus musculu
18	153	17.5	161	2	Q7TNI7	Q7tni7 mus musculu
19	153	17.5	161	2	AAQ88439	Aaq88439 mus muscu
20	148.5	17.0	153	1	I17F_HUMAN	Q96pd4 homo sapien
21	148.5	17.0	163	2	Q6NSI0	Q6nsio homo sapien
22	148.5	17.0	163	2	AAH70124	Aah70124 homo sapi
23	146	16.7	171	2	Q6L5M5	Q6l5m5 ciona intes
24	144	16.5	155	1	IL17_HUMAN	Q16552 homo sapien
25	144	16.5	155	2	AAH67503	Aah67503 homo sapi
26	144	16.5	155	2	AAH67504	Aah67504 homo sapi
27	144	16.5	155	2	AAH67505	Aah67505 homo sapi
28	143	16.4	169	2	Q7T1P7	Q7t1p7 gallus gall
29	137	15.7	155	2	Q6NZ94	Q6nz94 homo sapien
30	137	15.7	155	2	AAH66253	Aah66253 homo sapi
31	133.5	15.3	151	1	VG13_SHV21	P24916 saimiriine
32	131.5	15.1	151	1	VG13_SHV2C	O40633 saimiriine
33	131.5	15.1	151	2	Q778B0	Q778b0 saimiriine
34	131.5	15.1	151	2	CAC84308	Cac84308 saimiriin
35	130.5	15.0	141	2	Q95L56	Q95l56 bos taurus
36	130.5	15.0	186	2	Q6L5M4	Q6l5m4 ciona intes
37	124.5	14.3	153	2	Q8VHC9	Q8vhc9 mus musculu
38	124.5	14.3	169	2	Q8VHH8	Q8vhh8 mus musculu
39	124	14.2	150	1	IL17_RAT	Q61453 rattus norv
40	123.5	14.2	177	1	I17E_HUMAN	Q9h293 homo sapien
41	123.5	14.2	177	2	AAH69565	Aah69565 homo sapi
42	116.5	13.4	158	1	IL17_MOUSE	Q62386 mus musculu
43	116.5	13.4	158	2	BAC30590	Bac30590 mus muscu
44	105.5	12.1	2212	2	Q7Q112	Q7q112 anopheles g
45	104	11.9	146	2	Q70I21	Q70i21 oncorhynchu